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Supplemental Material

Characterization of Conserved Toxicogenomic Responses in Chemically Exposed Hepatocytes across Species and Platforms

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Table of Contents

All supplemental material are being hosted and maintained at a companion website <https://www.pmgenomics.ca/bhklab/pubs/tgates/>. This Table of Contents contains all the supplemental materials referenced within our manuscript. These are listed below:

Supplemental Material – Table 1: This table shows an approximated parent term extracted from the Reactome database for the conserved modules in RLV, PHH and PRH. Modules in all datasets are highlighted according to the following color scheme: Blue: module unique to one experimental setting (RLV, PRH or PHH); Yellow: conserved between RLV and PRH; Orange: conserved between PRH and PHH; Violet: conserved between PHH and RLV; and Green: conserved in all three experimental settings.

<https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/table1.pdf>

Supplemental Material – Figure S1: Venn diagram showing the overlap between human and rat Reactome pathways.

https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/Figure_S1.pdf

Supplemental Material – Figure S2: Zip file with all the histograms showing the distribution of significant differentially expressed genes in hepatocarcinogens vs. non hepatocarcinogens, in RLV, PRH and PHH respectively (False discovery rate < 10%).

https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/Figure_S2.zip

Supplemental Material – Common list of chemicals: One hundred and fifteen common chemicals analyzed in the TG-GATEs project. Among the experiments in TG-GATEs, these 115 chemicals were common for the rat *in vivo*, primary human hepatocytes, and primary rat hepatocytes platforms. This included known rat hepatocarcinogens. Non-carcinogenic compounds, selected as a negative control, are highlighted in blue.

<https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/chemicals.pdf>

Supplemental Material – S2: Zip file of all module heatmaps in RLV, PHH and PRH.

<https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/S2.zip>

Supplemental Material – S3: Zip file with xls files containing p-values of module overlaps (for all experimental settings), p-values for the 'special' cases such as hepatocarcinogens/cancer pathways/etc.

<https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/S3.zip>

Supplemental Material – S4: Zip file with all leading edge genes in all modules for all datasets.

<https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/S4.zip>

Supplemental Material – Reproducibility of analysis: Document describing how to reproduce the study results by running the analysis pipeline.

<https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/analysis.pdf>

All codes and R scripts are found on: <https://github.com/bhklab/TGGATES>

Normalized microarray data can be automatically obtained by running the pipeline, and these data are also available from here:

https://www.pmgenomics.ca/bhklab/sites/default/files/downloads/TGGATES_normalized_data.zip